

MARKED-UP VERSION OF AMENDMENTS

JC675 U.S. PRO
10/007132
12/03/01



Additions to the text are indicated by double underlining; deletions are indicated by square brackets.

In the Specification:

The replacement title on page 1, lines 4-5, and on page 236, line 1:

**-- [DNA ENCODING GALANIN GALR3 RECEPTORS AND USES THEREOF]
PROCESSES FOR PREPARING COMPOSITIONS INVOLVING GALR3
RECEPTOR SPECIFIC COMPOUNDS--**

The replacement paragraph on page 1, after the title:

-- This application is a continuation of U.S. Serial No. 09/058,333, filed April 9, 1998, now allowed, which is a continuation-in-part of PCT International Application No. PCT/US97/18222, filed October 9, 1997, which is a continuation-in-part [in the U.S.] and claims priority of U.S. Serial No. 08/900,230, filed July 23, 1997, now allowed, which is a continuation-in-part of U.S. Serial No. 08/787,261, filed January 24, 1997, now abandoned, which is a continuation-in-part of U.S. Serial No. 08/767,964, filed December 17, 1996, now abandoned, which is a continuation-in-part of U.S. Serial No. 08/728,139, filed October 9, 1996, now abandoned, the contents of which are incorporated by reference. Throughout this application, various references are referred to within parentheses. Disclosures of these publications in their entireties are hereby incorporated by reference into this application to more fully describe the state of the art to which this invention pertains. Full bibliographic citation for these references may be found at the end of this application, preceding the

Applicants: Jonathan A. Bard
Serial No: Not Yet Known
Filed: Herewith
Exhibit 1

sequence listing and the claims. --

The replacement paragraph on page 8, line 33 through page 9, line 9:

--This invention provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within one of the two strands of the nucleic acid encoding the GALR3 receptor contained in plasmid K1086. This invention still further provides a nucleic acid probe comprising 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within (a) the nucleic acid sequence described in Figure 1 ([Seq. ID No. 1] SEQ ID NO: 1) or (b) the reverse compliment to the nucleic acid sequence shown in Figure 1 ([Seq. ID No. 1] SEQ ID NO: 1).-

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The replacement paragraph on page 9, lines 11-33:

--In yet another embodiment, the GALR3 receptor is the rat GALR3 receptor having substantially the same amino acid sequence as the amino acid sequence shown in Figure 2. In another embodiment, the GALR3 receptor is the rat GALR3 receptor having the amino acid sequence shown in Figure 2. In another embodiment, the GALR3 receptor is the human GALR3 receptor. In another embodiment, the GALR3 receptor is the human GALR3 receptor encoded by the coding sequence of plasmid pEXJ-hGalR3. This invention also provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid

encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within one of the two strands of the nucleic acid encoding the GALR3 receptor contained in plasmid pEXJ-hGalR3. This invention provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within (a) the nucleic acid sequence described in Figure 3 ([Seq. ID No. 3] SEQ ID NO: 3) or (b) the reverse compliment to the nucleic acid sequence shown in Figure 3 ([Seq. ID No. 3] SEQ ID NO: 3).--

The replacement paragraph on page 24, lines 3-6:

--Figure 1 Nucleotide coding sequence of the rat hypothalamic galanin GALR3 receptor ([Seq. I.D. No. 1] SEQ ID NO: 1), with partial 5' and 3' untranslated sequences. Start and stop codons are underlined.--

The replacement paragraph on page 24, lines 7-10:

--Figure 2 Deduced amino acid sequence of the rat hypothalamic galanin GALR3 receptor ([Seq. I.D. No. 2] SEQ ID NO: 2) encoded by the rat nucleotide sequence shown in Figure 1.--

The replacement paragraph on page 24, lines 12-15:

--Figure 3 Nucleotide coding sequence of the human galanin GALR3 receptor ([Seq. I.D. No. 3] SEQ ID NO: 3), with partial 5' and 3' untranslated sequences. Start and stop codons are underlined.--

The replacement paragraph on page 24, lines 17-22:

--**Figure 4** Deduced amino acid sequence of the human galanin GALR3 receptor ([Seq. I.D. No. 4] SEQ ID NO: 4) encoded by the human nucleotide sequence shown in Figure 3.--

The replacement paragraph on page 24, lines 24-29:

--**Figures 5A-5D** Amino acid sequence alignment of the rat GALR3 receptor (top row) ([Seq. ID No. 2] SEQ ID NO: 2), human GALR3 receptor (middle row) ([Seq. ID No. 4] SEQ ID NO: 4) and rat GALR1 receptor (bottom row) ([Seq. ID No. 5] SEQ ID NO: 5). Transmembrane domains (TM 1-7) are indicated by brackets above the sequence.--

The replacement paragraph on page 29, line 13 through page 30, line 3:

---This invention provides an isolated nucleic acid encoding a GALR3 receptor having the same or substantially the same amino acid sequence as the amino acid sequence encoded by the plasmid K1086 (ATCC Accession No. 97747). In an embodiment, the nucleic acid is DNA. This invention further provides an isolated nucleic acid encoding a rat GALR3 receptor having the amino acid sequence encoded by the plasmid K1086. This invention provides an isolated nucleic acid encoding a GALR3 receptor having the same or substantially the same amino acid sequence as the amino acid sequence encoded by the plasmid pEXJ-RGalR3T (ATCC Accession No. 97826). In an embodiment, the nucleic acid is DNA. This invention further provides an isolated nucleic acid encoding a rat GALR3 receptor having the amino acid sequence encoded by the plasmid pEXJ-RGalR3T (ATCC Accession No. 97826). This invention provides an isolated nucleic acid encoding a GALR3 receptor having substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. I.D. No. 2] SEQ ID NO: 2). In

another embodiment, the GALR3 receptor is the rat GALR3 receptor having the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the nucleic acid comprises at least an intron. In still another embodiment, the nucleic acid comprises alternately spliced nucleic acid transcribed from the nucleic acid contained in plasmid K1086. In an embodiment, the alternately spliced nucleic acid is mRNA transcribed from DNA encoding a galanin receptor.--

The replacement paragraph on page 30, lines 5-18:

---In an embodiment, the GALR3 receptor is a human GALR3 receptor. This invention provides an isolated nucleic acid encoding a human GALR3 receptor having the same or substantially the same amino acid sequence as the amino acid sequence encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). This invention provides an isolated nucleic acid encoding a human GALR3 receptor, wherein the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 34, line 33 through page 35, line 10:

--This invention also provides an isolated galanin GALR3 receptor protein. In one embodiment, the GALR3 receptor protein has the same or substantially the same amino acid sequence as the amino acid sequence encoded by plasmid

K1086. In another embodiment, the GALR3 receptor protein has the amino acid sequence encoded by plasmid K1086. In another embodiment, the protein has the amino acid sequence encoded by the plasmid pEXJ-hGalR3. In an embodiment, the GALR3 receptor protein has the same or substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. I.D. No. 2] SEQ ID NO: 2). In an embodiment, the GALR3 receptor comprises the same or substantially the same amino acid sequence as the amino acid sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 38, lines 29-30:

--This invention provides a plasmid designated M67 (ATCC [Accession] Designation No. 209708).--

The replacement paragraph on page 38, line 32 through page 39, line 1:

--This plasmid (M67) was deposited on March 27, 1998, with the American Type Culture Collection (ATCC), [12301 Parklawn Drive, Rockville, Maryland 20852,] 10801 University Blvd., Manassas, Virginia 20110-2209, U.S.A. under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure and was accorded ATCC [Accession] Designation No. [xxxxx] 209708.--

The replacement paragraph on page 40, line 35 through page 41, line 5:

---This invention still further provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence

corresponding to a sequence present within (a) the nucleic acid sequence shown in Figure 1 ([Seq. ID No. 1] SEQ ID NO: 1) or (b) the reverse complement to the nucleic acid sequence shown in Figure 1 ([Seq. ID No. 1] SEQ ID NO: 1).--

The replacement paragraph on page 41, lines 7-20:

--This invention also provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within one of the two strands of the nucleic acid encoding the GALR3 receptor contained in plasmid pEXJ-hGalR3. This invention provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within (a) the nucleic acid sequence shown in Figure 3 ([Seq. ID No. 3] SEQ ID NO: 3) or (b) the reverse complement to the nucleic acid sequence shown in Figure 3 ([Seq. ID No. 3] SEQ ID NO: 3).--

The replacement paragraph on page 48, line 16 through 49, line 15:

--In one embodiment, the GALR3 receptor is a mammalian GALR3 receptor. In another embodiment, the GALR3 receptor is a rat GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid K1086. In still another embodiment, the GALR3 receptor has the amino acid sequence encoded by plasmid K1086. In another embodiment, the GALR3 receptor has substantially the same amino acid

sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In still another embodiment, the cells are transfected with the plasmid pEXJ-RGALR3T (ATCC Accession No. 97826), encoding the rat GALR3 receptor. Plasmid pEXJ-RGalR3T comprises the entire coding region of rat GALR3, but in which the 5' initiating ATG is joined directly to the vector, and which comprises only 100 nucleotides from the 3' untranslated region after the stop codon (i.e., up to and including nucleotide 1275 in Figure 1 ([Seq. ID NO. 1] SEQ ID NO: 1)). Transfection of cells with the "trimmed" plasmid results in a higher level of expression of the rat GALR3 receptor than the level of expression when plasmid K1086 is used. The use of the "trimmed" plasmid provides for greater convenience and accuracy in binding assays. In another embodiment the GALR3 receptor is a human GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In an embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 50, line 17 through 51, line 4:

---In one embodiment, the GALR3 receptor is a rat GALR3 receptor. In another embodiment, the GALR3 receptor has

the same or substantially the same amino acid sequence as that encoded by the plasmid K1086. In yet another embodiment, the GALR3 receptor has the amino acid sequence encoded by the plasmid K1086. In another embodiment, the GALR3 receptor has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor is a human GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 ATCC Accession No. 97827). In another embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment of this invention the cells are transfected with plasmid pEXJ-RGalR3T (ATCC Accession No. 97826).--

The replacement paragraph on page 51, line 29 through 52, line 15:

---In an embodiment, the GALR3 receptor is a mammalian GALR3 receptor. In one embodiment of the invention, the GALR3 receptor is a rat GALR3 receptor. In another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by the plasmid K1086. In still another embodiment, the GALR3 receptor has the amino acid sequence encoded by the plasmid K1086. In another embodiment, the GALR3 receptor

has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3_receptor is a human GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 ATCC Accession No. 97827). In another embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 53, lines 17-19:

--In an embodiment of any of the above processes, the cells are injected with RNA synthesized in vitro from the plasmid designated M67 (ATCC [Accession] Designation No. 209708).--

The replacement paragraph on page 58, line 34 through 59, line 21:

---In an embodiment of any of the above processes, the GALR3 receptor is a mammalian GALR3 receptor. In another embodiment of the above processes, the GALR3 receptor is a rat GALR3 receptor or a human GALR3 receptor. In still another embodiment of the above processes, the GALR3 receptor has the same or substantially the same amino acid sequence as encoded by the plasmid K1086 (ATCC Accession

No. 97747). In another embodiment, the GALR3 receptor has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In another embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment of this invention the cells are transfected with plasmid pEXJ-RGalR3T (ATCC Accession No. 97826).--

The replacement paragraph on page 61, line 20 through 62, line 5:

---In an embodiment of any of the above processes, the GALR3 receptor is a mammalian GALR3 receptor. In an embodiment of the above-described methods, the GALR3 receptor is a rat GALR3 receptor. In another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as the amino acid sequence encoded by plasmid K1086. In another embodiment, the GALR3 receptor has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor is a human GALR3 receptor. In still another embodiment, the

GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In another embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 63, lines 5-26:

---In an embodiment of any of the above-described methods, the GALR3 receptor is a rat GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as the amino acid sequence encoded by plasmid K1086. In another embodiment, the GALR3 receptor has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor is a human GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3

receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 64, line 33 through page 65, line 26:

--In an embodiment of any of the above-described methods, the GALR3 receptor is a rat GALR3 receptor. In another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as the amino acid sequence encoded by plasmid K1086. In another embodiment, the GALR3 receptor has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor is a human GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-RGalR3T (ATCC Accession No. 97826). In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid M54 (ATCC Accession No. 209312). In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid M67 (ATCC [Accession] Designation No. 209708). In another embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor

has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID NO. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 68, line 32 through page 69, line 15:

--In an embodiment of any of the above-described processes, the GALR3 receptor is a mammalian GALR3 receptor. In another embodiment of any of the above-described processes, the GALR3 receptor has substantially the same amino acid as encoded by the plasmid K1086 (ATCC Accession No. 97747). In another embodiment of any of the above-described processes, the GALR3 receptor has substantially the same amino acid sequence as that shown in Figure 2 ([Seq. ID NO. 2] SEQ ID NO: 2). In still another embodiment of any of the above-described processes, the GALR3 receptor has substantially the same amino acid sequence as encoded by the plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In an embodiment of any of the above-described processes, the GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as that shown in Figure 4 ([Seq. ID NO. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In still another embodiment of any of the above-described processes, the GALR3 receptor has a sequence, which sequence comprises a sequence shown in Figure 4 ([Seq. ID NO. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 98, lines 7-18:

--Human brain multiple tissue northern blots (MTN brain blots II and III, Clontech, Palo Alto, CA) and human peripheral MTN blot (Clontech, Palo Alto, CA) carrying mRNA

(2 µg) purified from various human brain areas and peripheral tissues, respectively, were hybridized at high stringency with overlapping probes directed to the amino-terminus of hGALR3

5' GATGGCTGATGCCAGAACATTCACTGGACAGCCCAGGGAGTGT 3'

([SEQ ID NO. 51] SEQ ID NO: 51) and

5' GACCACAGGCAGTGCACGGCCCCACACTCCCTGGGCTGTCCAG 3'

([SEQ ID NO. 52] SEQ ID NO: 52), according to the manufacturer's specifications.--

The replacement paragraph on page 98, lines 21-34:

--Tissues were homogenized and total RNA extracted using the guanidine isothiocyanate/CsCl cushion method. RNA was then treated with DNase to remove any contaminating genomic DNA and poly A⁺-selected using FastTrack kit (Invitrogen), according to manufacturer's specifications. cDNA was prepared from mRNA with random hexanucleotide primers using reverse transcriptase Superscript II (BRL, Gaithersburg, MD). First strand cDNA (corresponding to ≈5 ng of poly A⁺ RNA) was amplified in a 50 µL PCR reaction mixture with 300 nM of forward (directed to the amino-terminus: ([SEQ ID NO. 24] SEQ ID NO: 24) and reverse (directed to the third intracellular loop: ([SEQ ID NO. 27] SEQ ID NO: 27)) primers, using the thermal cycling program and conditions described above.--

The replacement paragraph on page 98, line 37 through page 99, line 13:

--The PCR products were run on a 1.5% agarose gel and transferred to charged nylon membranes (Zetaprobe GT, BioRad), and analyzed as Southern blots. GALR3 primers were screened for the absence of cross-reactivity with the other galanin receptors. Filters were hybridized with a

radiolabeled probe directed to the first intracellular loop,

5'-TGCAGCCTGGCCCAAGTGCCTGGCAGGAGCCAAGCAGTACCAACAG-3' ([Seq. I.D. No. 53] SEQ ID NO: 53), and washed under high stringency. Labeled PCR products were visualized on X-ray film. Similar PCR and Southern blot analyses were conducted with primers and probes directed to the housekeeping gene, glyceraldehyde phosphate dehydrogenase (G3PDH; Clontech, Palo Alto, CA), to normalize the amount of cDNA used from the different tissues.--

The replacement paragraph on page 99, lines 15-27:

--RT-PCR was performed on human pituitary cDNA (two sources: Clontech cDNA and cDNA prepared from poly A+RNA purchased from ABS) using the following conditions: 94°C for 30 sec and 68°C for 2 min, for 40 cycles, with a preincubation at 94°C for 2 min and a postincubation at 68°C for 5 minutes. Primers specific for human GALR1 were used (KS1177; [SEQ ID NO. 35] SEQ ID NO: 35 and KS1178; [SEQ ID NO. 36] SEQ ID NO: 36). Primers specific for human GALR2 were used (BB183; [SEQ ID NO. 60] SEQ ID NO: 60 and BB184; [SEQ ID NO. 61] SEQ ID NO: 61). Primers specific for human GALR3 were used (BB444; [SEQ ID NO. 62] SEQ ID NO: 62 and BB445; [SEQ ID NO. 63] SEQ ID NO: 63). Primers specific for human prolactin were used (BB446; [SEQ ID NO. 64] SEQ ID NO: 64 and BB447; [SEQ ID NO. 65] SEQ ID NO: 65).--

The replacement paragraph on page 99, line 31 through page 100, line 8:

--BB183: 5'-TCAGCGGCACCATGAACGTCTCGGGCT-3' ([SEQ ID NO. 60] SEQ ID NO: 60).

BB184: 5'-GGCCACATCAACCGTCAGGATGCT-3' ([SEQ ID NO. 61]

SEQ ID NO: 61)

BB444: 5' -ATGGCTGATGCCAGAACATTCAC-3' ([SEQ ID NO. 62]
SEQ ID NO: 62).

BB445: 5' -TAGCGCACGGTGCCGTAGTAGCTGAGGT-3' ([SEQ ID NO. 63] SEQ ID NO: 63).

BB446: 5' -ATGAAAGGGTCCCTCCTGCTGCTGCT-3' ([SEQ ID NO. 64]
SEQ ID NO: 64).

BB447: 5' -TATCAGCTCCATGCCCTCTAGAAGCC-3' ([SEQ ID NO. 65]
SEQ ID NO: 65).--

The replacement paragraph on page 110, line 22 through page 112, line 10:

--Oocytes were isolated as described above, except that 3 mg/mL collagenase was used to defolliculate the oocytes. Genes encoding G-protein inwardly rectifying K⁺ channels 1 and 4 (GIRK1 and GIRK4) were obtained by PCR using the published sequences (Kubo et al., 1993; Dascal et al., 1993; Krapivinsky et al., 1995b) to derive appropriate 5' and 3' primers. Human heart cDNA was used as template together with the primers

5' -CGCGGATCCATTATGTCTGCCTCCGAAGGAAATTG-3' (SEQ ID NO[.]54) and

5' -CGCGAATTCTTATGTGAAGCGATCAGAGTTCTTTTC -3' (SEQ ID NO[.]55) for GIRK1 and

5' -GCGGGATCCGCTATGGCTGGTATTCTAGGAATG-3' (SEQ ID NO[.]56) and

5' - CCGGAATTCCCCCTCACACCGAGCCCCCTGG-3' (SEQ ID NO[.]57) for GIRK4. In each primer pair, the upstream primer contained a BamHI site and the downstream primer contained an EcoRI site to facilitate cloning of the PCR product into pcDNA1-Amp (Invitrogen). The transcription template for hGalR3 was obtained similarly by PCR using the cloned cDNA in

combination with primers

5'-CCAAGCTTCTAATACGACTCACTATAGGCCACCATGGCTGATGCCAGA-3'

(SEQ ID NO[.]58) and

5'-TTTTTTTTTTTTTTTTTTTTTTTTGCAGGG

TTTATTCCGGTCCTCG-3' (SEQ ID NO[.]59). Alternatively, the complete coding region of hGalR3 is subcloned into the high-efficiency transcription vector pBS KS⁺ AMV-pA50 (Nowak et al., 1995). This plasmid was modified by adding the recognition sequence for the restriction enzyme SrfI downstream of the poly A sequence in the plasmid. The new plasmid was designated M52. Subcloning involved the isolation of a 1.1 kb NcoI/EcoRI restriction fragment encoding the entire hGALR3 gene followed by its ligation into NcoI/EcoRI digested M52. After identification of a suitable clone (M54), the transcription template was produced by linearization of the plasmid DNA with SrfI. The plasmid M54 was deposited on September 30, 1997, with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland 20852, U.S.A. under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure and was accorded ATCC Accession No. 209312. The sequence comprising the coding region of rat GALR3 was subcloned into pBS KS⁺AMV-pA50 (Nowak, et al., 1995) to produce M67. The transcription template was produced by linearization of the plasmid DNA with SrfI. The plasmid M67 was deposited on March 27, 1998, with the American Type Culture Collection (ATCC), [12301 Parklawn Drive, Rockville, Maryland 20852,] 10801 University Blvd., Manassas, Virginia 20110-2209, U.S.A. under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure and was accorded ATCC [Accession] Designation No. [xxxxxx] 209708. mRNAs were transcribed using the T7 polymerase ("Message Machine", Ambion). Each oocyte received 2 ng each of GIRK1 and GIRK4

mRNA in combination with 25 ng of GalR3 mRNA. In other experiments oocytes received injections of mRNAs encoding the human α 1A adrenergic receptor, rGalR1 or rGalR2 galanin receptors (Forray et al., 1994; Parker et al., 1995) with or without GIRKs 1 and 4. After injection of mRNAs, oocytes were incubated at 17° for 3-8 days.--

The replacement paragraph on page 156, lines 12-23:

--The human GALR3 gene contains two in-frame METs: the first (as one reads 5' to 3') will be referred to herein as the "upstream MET" and the second (i.e., closer to TM1) will be referred to herein as the "downstream MET." Both the upstream and downstream METs are shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4). Based on data currently available, it is believed that the downstream MET is likely to be the correct initiating methionine. It is theoretically possible that the upstream MET might be the initiating MET. It is to be understood that the present invention includes both the receptor beginning at the downstream MET and the receptor beginning at the upstream MET.--

SEQUENCE LISTING

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(1) GENERAL INFORMATION:

- (i) APPLICANT: Bard, Jonathan A
Borowsky, Beth
Smith, Kelli E
- (ii) TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 65

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- (C) CITY: New York
- (D) STATE: New York
- (E) COUNTRY: U.S.A.
- (F) ZIP: 10036

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: White, John P
- (B) REGISTRATION NUMBER: 28,678
- (C) REFERENCE/DOCKET NUMBER: 52241-E/JPW/KDB

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 212 278 0400
- (B) TELEFAX: 212 391 0525

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 63..1172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCTCCAGCC TAGGCGTTCT ACCTGGAAGA ATGCAGGGGC CCAGTACCTA GGACTGAGGA 60

AG ATG GCT GAC ATC CAG AAC ATT TCG CTG GAC AGC CCA GGG AGC GTA 107

Applicants: Jonathan A. Bard et al.
Serial No: Not Yet Known
Filed: Herewith
Exhibit 2

Met Ala Asp Ile Gln Asn Ile Ser Leu Asp Ser Pro Gly Ser Val	1	5	10	15	
Gly Ala Val Ala Val Pro Val Ile Phe Ala Leu Ile Phe Leu Leu Gly	20	25	30		155
ATG GTG GGC AAT GGG CTG GTG TTG GCT GTG CTA CTG CAG CCT GGC CCA					203
Met Val Gly Asn Gly Leu Val Ala Val Leu Leu Gln Pro Gly Pro	35	40	45		
AGT GCC TGG CAG GAG CCA AGC AGT ACC ACA GAT CTC TTC ATC CTC AAC					251
Ser Ala Trp Gln Glu Pro Ser Ser Thr Thr Asp Leu Phe Ile Leu Asn	50	55	60		
TTG GCC GTG GCC GAC CTT TGC TTC ATC CTG TGC GTG CCC TTC CAG					299
Leu Ala Val Ala Asp Leu Cys Phe Ile Leu Cys Cys Val Pro Phe Gln	65	70	75		
GCA GCC ATC TAC ACA CTG GAT GCC TGG CTC TTT GGG GCT TTC GTG TGC					347
Ala Ala Ile Tyr Thr Leu Asp Ala Trp Leu Phe Gly Ala Phe Val Cys	80	85	90	95	
AAG ACG GTA CAT CTG CTC ATC TAC CTC ACC ATG TAT GCC AGC AGC TTC					395
Lys Thr Val His Leu Leu Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe	100	105	110		
ACC CTG GCG GCC GTC TCC CTG GAC AGG TAC CTG GCT GTG CGG CAC CCA					443
Thr Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala Val Arg His Pro	115	120	125		
CTG CGC TCC AGA GCC CTG CGC ACC CCG CGC AAC GCG CGC GCC GCC GTG					491
Leu Arg Ser Arg Ala Leu Arg Thr Pro Arg Asn Ala Arg Ala Ala Val	130	135	140		
GGG CTC GTG TGG CTG CTG GCG GCT CTC TTT TCC GCG CCC TAC CTA AGC					539
Gly Leu Val Trp Leu Leu Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser	145	150	155		
TAT TAC GGC ACG GTG CGC TAC GGC GCG CTC GAG CTC TGC GTG CCC GCT					587
Tyr Tyr Gly Thr Val Arg Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala	160	165	170	175	
TGG GAG GAC GCG CGG CGG CGC GCG CTG GAC GTG GCC ACC TTC GCC GCG					635
Trp Glu Asp Ala Arg Arg Ala Leu Asp Val Ala Thr Phe Ala Ala	180	185	190		
GGC TAC CTG CTG CCG GTG GCC GTG AGC CTG GCC TAC GGA CGC ACG					683
Gly Tyr Leu Leu Pro Val Ala Val Val Ser Leu Ala Tyr Gly Arg Thr	195	200	205		
CTA TGT TTC CTA TGG GCC GCC GTG GGT CCC GCG GGC GCG GCG GCA GCA					731
Leu Cys Phe Leu Trp Ala Ala Val Gly Pro Ala Gly Ala Ala Ala	210	215	220		
GAG GCG CGC AGA CGG GCG ACC GGC CGG GCG GGA CGC GCC ATG CTG GCA					779
Glu Ala Arg Arg Ala Thr Gly Arg Ala Gly Arg Ala Met Leu Ala	225	230	235		
GTG GCC GCG CTC TAC GCG CTT TGC TGG GGC CCG CAC CAC GCG CTC ATC					827
Val Ala Ala Leu Tyr Ala Leu Cys Trp Gly Pro His His Ala Leu Ile	240	245	250	255	

CTC TGC TTC TGG TAC GGC CGC TTC GCC TTC AGC CCG GCC ACC TAC GCC Leu Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala 260 265 270	875
TGT CGC CTG GCC TCG CAC TGC CTC GCC TAC GCC AAC TCC TGC CTT AAC Cys Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn 275 280 285	923
CCG CTC GTC TAC TCG CTC GCC TCG CGC CAC TTC CGC GCG CGC TTC CGC Pro Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg 290 295 300	971
CGC CTG TGG CCC TGC GGC CGT CGC CGC CAC CGC CAC CAC CGC GCT Arg Leu Trp Pro Cys Gly Arg Arg His Arg His His His Arg Ala 305 310 315	1019
CAT CGA GCC CTC CGT GTC CAG CCG GCG TCT TCG GGC CCC GCC GGT His Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly 320 325 330 335	1067
TAT CCC GGC GAC GCC AGG CCT CGT GGT TGG AGT ATG GAG CCC AGA GGG Tyr Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly 340 345 350	1115
GAT GCT CTG CGT GGT GGT GGA GAG ACT AGA CTA ACC CTG TCC CCC AGG Asp Ala Leu Arg Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg 355 360 365	1163
GGA CCT CAA TAACCCTGCC CGCTTGGACT CTGACGTCTG TCAGAATGCC Gly Pro Gln 370	1212
ACCAAGGAAC ATCTAGGGAA CGGCAGTCTC GCCAGGCTCC ACCAAAAAGC AGAAGCAAAG	1272
TTGCAGGG	1280

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asp Ile Gln Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly 1 5 10 15
Ala Val Ala Val Pro Val Ile Phe Ala Leu Ile Phe Leu Leu Gly Met 20 25 30
Val Gly Asn Gly Leu Val Leu Ala Val Leu Leu Gln Pro Gly Pro Ser 35 40 45
Ala Trp Gln Glu Pro Ser Ser Thr Thr Asp Leu Phe Ile Leu Asn Leu 50 55 60
Ala Val Ala Asp Leu Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala 65 70 75 80

Ala Ile Tyr Thr Leu Asp Ala Trp Leu Phe Gly Ala Phe Val Cys Lys
85 90 95

Thr Val His Leu Leu Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe Thr
100 105 110

Leu Ala Ala Val Ser Leu Asp Arg Tyr Leu Ala Val Arg His Pro Leu
115 120 125

Arg Ser Arg Ala Leu Arg Thr Pro Arg Asn Ala Arg Ala Ala Val Gly
130 135 140

Leu Val Trp Leu Leu Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser Tyr
145 150 155 160

Tyr Gly Thr Val Arg Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala Trp
165 170 175

Glu Asp Ala Arg Arg Ala Leu Asp Val Ala Thr Phe Ala Ala Gly
180 185 190

Tyr Leu Leu Pro Val Ala Val Val Ser Leu Ala Tyr Gly Arg Thr Leu
195 200 205

Cys Phe Leu Trp Ala Ala Val Gly Pro Ala Gly Ala Ala Ala Ala Glu
210 215 220

Ala Arg Arg Arg Ala Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val
225 230 235 240

Ala Ala Leu Tyr Ala Leu Cys Trp Gly Pro His His Ala Leu Ile Leu
245 250 255

Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys
260 265 270

Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro
275 280 285

Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg
290 295 300

Leu Trp Pro Cys Gly Arg Arg His Arg His His His Arg Ala His
305 310 315 320

Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly Tyr
325 330 335

Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly Asp
340 345 350

Ala Leu Arg Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg Gly
355 360 365

Pro Gln
370

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1417 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAC TCA GCG ATG ACT TTG GCT CTG CTC TCC CCT CCT CCA TCT CCC ACG	48
His Ser Ala Met Thr Leu Ala Leu Leu Ser Pro Pro Pro Ser Pro Thr	
375 380 385	
AGC TTC CAG CCC AGA ACA CCT GGC CAG ACC CAG GTC GGG GGA GTT AGA	96
Ser Phe Gln Pro Arg Thr Pro Gly Gln Thr Gln Val Gly Gly Val Arg	
390 395 400	
TCC CGG GGT CAA GCA ACC AGA ACT GGG GGC TCT TGC CTG AGG ATT CCA	144
Ser Arg Gly Gln Ala Thr Arg Thr Gly Gly Ser Cys Leu Arg Ile Pro	
405 410 415	
GCT TCT CTT CCC AGG TGC CCG TCT GAT GGG GAG ATG GCT GAT GCC CAG	192
Ala Ser Leu Pro Arg Cys Pro Ser Asp Gly Glu Met Ala Asp Ala Gln	
420 425 430	
AAC ATT TCA CTG GAC AGC CCA GGG AGT GTG GGG GCC GTG GCA GTG CCT	240
Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly Ala Val Ala Val Pro	
435 440 445 450	
GTG GTC TTT GCC CTA ATC TTC CTG CTG GGC ACA GTG GGC AAT GGG CTG	288
Val Val Phe Ala Leu Ile Phe Leu Leu Gly Thr Val Gly Asn Gly Leu	
455 460 465	
GTG CTG GCA GTG CTC CTG CAG CCT GGC CCG AGT GCC TGG CAG GAG CCT	336
Val Leu Ala Val Leu Leu Gln Pro Gly Pro Ser Ala Trp Gln Glu Pro	
470 475 480	
GGC AGC ACC ACG GAC CTG TTC ATC CTC AAC CTG GCG GTG GCT GAC CTC	384
Gly Ser Thr Asp Leu Phe Ile Leu Asn Leu Ala Val Ala Asp Leu	
485 490 495	
TGC TTC ATC CTG TGC GTG CCC TTC CAG GCC ACC ATC TAC ACG CTG	432
Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala Thr Ile Tyr Thr Leu	
500 505 510	
GAT GCC TGG CTC TTT GGG GCC CTC GTC TGC AAG GCC GTG CAC CTG CTC	480
Asp Ala Trp Leu Phe Gly Ala Leu Val Cys Lys Ala Val His Leu Leu	
515 520 525 530	
ATC TAC CTC ACC ATG TAC GCC AGC AGC TTT ACG CTG GCT GCT GTC TCC	528
Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe Thr Leu Ala Ala Val Ser	
535 540 545	
GTG GAC AGG TAC CTG GCC GTG CGG CAC CCG CTG CGC TCG CGC GCC CTG	576
Val Asp Arg Tyr Leu Ala Val Arg His Pro Leu Arg Ser Arg Ala Leu	
550 555 560	
CGC ACG CCG CGT AAC GCC CGC GCC GCA GTG GGG CTG GTG TGG CTG CTG	624

Arg Thr Pro Arg Asn Ala Arg Ala Ala Val Gly Leu Val Trp Leu Leu		
565	570	575
GCG GCG CTC TTC TCG GCG CCC TAC CTC AGC TAC TAC GGC ACC GTG CGC		672
Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser Tyr Tyr Gly Thr Val Arg		
580	585	590
TAC GGC GCG CTG GAG CTC TGC GTG CCC GCC TGG GAG GAC GCG CGC CGC		720
Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala Trp Glu Asp Ala Arg Arg		
595	600	605
CGC GCC CTG GAC GTG GCC ACC TTC GCT GCC GGC TAC CTG CTG CCC GTG		768
Arg Ala Leu Asp Val Ala Thr Phe Ala Ala Gly Tyr Leu Leu Pro Val		
615	620	625
GCT GTG GTG AGC CTG GCC TAC GGG CGC ACG CTG CGC TTC CTG TGG GCC		816
Ala Val Val Ser Leu Ala Tyr Gly Arg Thr Leu Arg Phe Leu Trp Ala		
630	635	640
GCC GTG GGT CCC GCG GGC GCG GCG GCG GCG GAG GCG CGG CGG AGG GCG		864
Ala Val Gly Pro Ala Gly Ala Ala Ala Glu Ala Arg Arg Arg Arg Ala		
645	650	655
ACG GGC CGC GCG GGG CGC GCC ATG CTG GCG GTG GCC GCG CTC TAC GCG		912
Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val Ala Ala Leu Tyr Ala		
660	665	670
CTC TGC TGG GGT CCG CAC CAC GCG CTC ATC CTG TGC TTC TGG TAC GGC		960
Leu Cys Trp Gly Pro His His Ala Leu Ile Leu Cys Phe Trp Tyr Gly		
675	680	685
CGC TTC GCC TTC AGC CCG GCC ACC TAC GCC TGC CGC CTG GCC TCA CAC		1008
Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys Arg Leu Ala Ser His		
695	700	705
TGC CTG GCC TAC GCC AAC TCC TGC CTC AAC CCG CTC GTC TAC GCG CTC		1056
Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro Leu Val Tyr Ala Leu		
710	715	720
GCC TCG CGC CAC TTC CGC GCG CGC TTC CGC CGC CTG TGG CCG TGC GGC		1104
Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg Leu Trp Pro Cys Gly		
725	730	735
CGC CGA CGC CGC CAC CGT GCC CGC CGC GCC TTG CGT CGC GTC CGC CCC		1152
Arg Arg Arg Arg His Arg Ala Arg Arg Ala Leu Arg Arg Val Arg Pro		
740	745	750
GCG TCC TCG GGC CCA CCC GGC TGC CCC GGA GAC GCC CGG CCT AGC GGG		1200
Ala Ser Ser Gly Pro Pro Gly Cys Pro Gly Asp Ala Arg Pro Ser Gly		
755	760	765
AGG CTG CTG GCT GGT GGC GGC CAG GGC CCG GAG CCC AGG GAG GGA CCC		1248
Arg Leu Leu Ala Gly Gly Gln Gly Pro Glu Pro Arg Glu Gly Pro		
775	780	785
GTC CAC GGC GGA GAG GCT GCC CGA GGA CCG GAA TAAACCCCTGC CGCCTGGACT		1301
Val His Gly Gly Glu Ala Ala Arg Gly Pro Glu		
790	795	
CCGCCTGTGT CCGTCTGTCT CACTCCGTT CTCCGAAGGC GGGACGCCAC CGGGCCAGGG		1361
ATGGGGCAAT GCCACGAGCT CTCTGAGGGG CGTTGAGTGG AGCGACTTGT CCCCCGC		1417

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 427 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

His Ser Ala Met Thr Leu Ala Leu Leu Ser Pro Pro Pro Pro Ser Pro Thr
1 5 10 15

Ser Phe Gln Pro Arg Thr Pro Gly Gln Thr Gln Val Gly Gly Val Arg
20 25 30

Ser Arg Gly Gln Ala Thr Arg Thr Gly Gly Ser Cys Leu Arg Ile Pro
35 40 45

Ala Ser Leu Pro Arg Cys Pro Ser Asp Gly Glu Met Ala Asp Ala Gln
50 55 60

Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly Ala Val Ala Val Pro
65 70 75 80

Val Val Phe Ala Leu Ile Phe Leu Leu Gly Thr Val Gly Asn Gly Leu
85 90 95

Val Leu Ala Val Leu Leu Gln Pro Gly Pro Ser Ala Trp Gln Glu Pro
100 105 110

Gly Ser Thr Thr Asp Leu Phe Ile Leu Asn Leu Ala Val Ala Asp Leu
115 120 125

Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala Thr Ile Tyr Thr Leu
130 135 140

Asp Ala Trp Leu Phe Gly Ala Leu Val Cys Lys Ala Val His Leu Leu
145 150 155 160

Ile Tyr Leu Thr Met Tyr Ala Ser Ser Phe Thr Leu Ala Ala Val Ser
165 170 175

Val Asp Arg Tyr Leu Ala Val Arg His Pro Leu Arg Ser Arg Ala Leu
180 185 190

Arg Thr Pro Arg Asn Ala Arg Ala Ala Val Gly Leu Val Trp Leu Leu
195 200 205

Ala Ala Leu Phe Ser Ala Pro Tyr Leu Ser Tyr Tyr Gly Thr Val Arg
210 215 220

Tyr Gly Ala Leu Glu Leu Cys Val Pro Ala Trp Glu Asp Ala Arg Arg
225 230 235 240

Arg Ala Leu Asp Val Ala Thr Phe Ala Ala Gly Tyr Leu Leu Pro Val
245 250 255

Ala Val Val Ser Leu Ala Tyr Gly Arg Thr Leu Arg Phe Leu Trp Ala
260 265 270

Ala Val Gly Pro Ala Gly Ala Ala Ala Ala Glu Ala Arg Arg Arg Ala
275 280 285

Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val Ala Ala Leu Tyr Ala
290 295 300

Leu Cys Trp Gly Pro His His Ala Leu Ile Leu Cys Phe Trp Tyr Gly
305 310 315 320

Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys Arg Leu Ala Ser His
325 330 335

Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro Leu Val Tyr Ala Leu
340 345 350

Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg Leu Trp Pro Cys Gly
355 360 365

Arg Arg Arg Arg His Arg Ala Arg Arg Ala Leu Arg Arg Val Arg Pro
370 375 380

Ala Ser Ser Gly Pro Pro Gly Cys Pro Gly Asp Ala Arg Pro Ser Gly
385 390 395 400

Arg Leu Leu Ala Gly Gly Gln Gly Pro Glu Pro Arg Glu Gly Pro
405 410 415

Val His Gly Gly Glu Ala Ala Arg Gly Pro Glu
420 425

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Leu Ala Pro Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro
1 5 10 15

Glu Pro Pro Ala Glu Pro Arg Pro Leu Phe Gly Ile Gly Val Glu Asn
20 25 30

Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val Leu
35 40 45

Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly Lys
50 55 60

Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala Asp
65 70 75 80

Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr Ala
85 90 95

Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His Tyr

100	105	110
Phe Phe Thr Val Ser Met Leu Val Ser Ile Phe Thr Leu Ala Ala Met		
115	120	125
Ser Val Asp Arg Tyr Val Ala Ile Val His Ser Arg Arg Ser Ser Ser		
130	135	140
Leu Arg Val Ser Arg Asn Ala Leu Leu Gly Val Gly Phe Ile Trp Ala		
145	150	155
Leu Ser Ile Ala Met Ala Ser Pro Val Ala Tyr Tyr Gln Arg Leu Phe		
165	170	175
His Arg Asp Ser Asn Gln Thr Phe Cys Trp Glu His Trp Pro Asn Gln		
180	185	190
Leu His Lys Lys Ala Tyr Val Val Cys Thr Phe Val Phe Gly Tyr Leu		
195	200	205
Leu Pro Leu Leu Leu Ile Cys Phe Cys Tyr Ala Lys Val Leu Asn His		
210	215	220
Leu His Lys Lys Leu Lys Asn Met Ser Lys Lys Ser Glu Ala Ser Lys		
225	230	235
Lys Lys Thr Ala Gln Thr Val Leu Val Val Val Val Phe Gly Ile		
245	250	255
Ser Trp Leu Pro His His Val Ile His Leu Trp Ala Glu Phe Gly Ala		
260	265	270
Phe Pro Leu Thr Pro Ala Ser Phe Phe Phe Arg Ile Thr Ala His Cys		
275	280	285
Leu Ala Tyr Ser Asn Ser Ser Val Asn Pro Ile Ile Tyr Ala Phe Leu		
290	295	300
Ser Glu Asn Phe Arg Lys Ala Tyr Lys Gln Val Phe Lys Cys Arg Val		
305	310	315
Cys Asn Glu Ser Pro His Gly Asp Ala Lys Glu Lys Asn Arg Ile Asp		
325	330	335
Thr Pro Pro Ser Thr Asn Cys Thr His Val		
340	345	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGTACCCCT ATTTTCGCG CTCATCTTCC TCGTGGGCAC CGTGG

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGCACCGCCA GCACCAGCGC GTTGCCCACG GTGCCACGA GGAAG

45

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCAGCACCAC CAACCTGTTCAATCCTCAACC TGGGCGTGGCGACCTGTGT

50

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCCTGGAAA GGCACGCAGC ACAGGATGAA ACACAGGTCG GCCACGCCA

50

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGCAAGGCT GTTCATTTCC TCATCTTCT CACTATGCAC GCCAG

45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAGACGGCG GCCAGCGTGA AGCTGCTGGC GTGCATAGTG AGAAA

45

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AACCGCGCTGG CCGCCATCGG GCTCATCTGG GGGCTAGCAC TGCTC

45

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGTAGCTCAG GTAGGGCCCG GAGAAGAGCA GTGCTAGCCC CCAGA

45

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCCATGGAC CTCTGCACCT TCGTCTTAG CTACCTGCTG CCAGT

45

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCATAGGTC AGACTGAGGA CTAGCACTGG CAGCAGGTAG CTAAA

45

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCATCATC GTGGCGGTGC TTTTCTGCCT CTGTTGGATG CCCCCA

45

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACACGCAG AGGATAAGCG CGTGGTGGGG CATCCAACAG AGGCA

45

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTGCGCATC CTTTCACACC TAGTTCTTA TGCCAACTCC TGTGT

45

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGACCAGAGC GTAAACGATG GGGTTGACAC AGGAGTTGGC ATAGGA

46

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTCAGTGAA GGGAAATGGGA GCGA

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTAGTGTATA AACTTGCAGA TGAAGGC

27

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAATGGCT CCGGCAGCCA GGG

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGCAGAGCA GCGAGCCGAA CAC

23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCTGACATC CAGAACATTT CGCT

24

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAGATGTACC GTCTTGCACA CGAA

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CATCTGCTCA TCTACCTCAC CATG

24

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATAGGAAAC ATAGCGTGCG TCCG

24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTTCTAG AGATCCCTCG ACCTC

25

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGGCGCAGAA CTGGTAGGTA TGGAA

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCTCATCCTC TGCTTCTGGT ACG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGATGTACC GTCTTGCACA CGAA 24

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGAGGATCCC AACTTGCCT CTGCTTTTG GTGG 34

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCTCAGTGAA GGGAAATGGGA GCGA 24

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTTGCTTGTA CGCCTTCCGG AAGT 24

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
TGGGCAACAG CCTAGTGATC ACCG 24

(2) INFORMATION FOR SEQ ID NO:36:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
CTGCTCCCAG CAGAAGGTCT GGTT 24

(2) INFORMATION FOR SEQ ID NO:37:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
ATGAATGGCT CCGGCAGCCA GGG 23

(2) INFORMATION FOR SEQ ID NO:38:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
TTGGAGACCA GAGCGTAAAC GATGG 25

(2) INFORMATION FOR SEQ ID NO:39:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGATGGCTGA CATCCAGAAC ATTCGCTGG ACAGCCCAGG GAGCG

45

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATCACAGGCA CTGCCACAGC CCCTACGCTC CCTGGGCTGT CCAGCG

46

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGGCTGATG CCCAGAACAT TTCAC

25

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AGCCAGGCAT CCAGCGTGT GAT

23

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACGGTCGCTT CGCCTTCAGC CCGGCCACCT ACGCCTGTCG CCTGG

45

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACGGTCGCTT CGCCTTCAGC CCGGCCACCT ACGCCTGTCG CCTGG

45

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCGCAACGCG CGCGCCGCCG TGGGGCTCGT GTGGCTGCTG GCGGC

45

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTACACGC TGGATGCCTG GCTCTTGCG GCCCTCGTCT GCAAG

45

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATCTACACGC TGGATGCCCT GGCT

24

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGTAGCGCAC GGTGCCGTAG TA

22

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATGGATCCG CCACCATGGC TGATGCCAG AACATTCAC

40

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAGGGTACCT GTCCACGGAG ACAGCAGC

28

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATGGCTGAT GCCCAGAACCA TTTCACTGGA CAGCCCAGGG AGTGT

45

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GACCACAGGC ACTGCCACGG CCCCCACACT CCCTGGGCTG TCCAG

45

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGCAGCCTGG CCCAAGTGCC TGGCAGGAGC CAAGCAGTAC CACAG

45

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGCGGATCCA TTATGTCTGC ACTCCGAAGG AAATTTG

37

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGCGAATTCT TATGTGAAGC GATCAGAGTT CATTTC

38

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCAGGGATCCG CTATGGCTGG TGATTCTAGG AATG

34

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCGGAATTCC CCTCACACCG AGCCCCTGG

29

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCAAGCTTCT AATACGACTC ACTATAGGGC CACCATGGCT GATGCCAGA

50

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTGCAGG GTTTATTCCG GTCCTCG

57

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TCAGCGGCAC CATGAACGTC TCAGGCT

27

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGCCACATCA ACCGTCAGGA TGCT

24

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATGGCTGATG CCCAGAACAT TTCAC

25

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAGCGCACGG TGCCGTAGTA GCTGAGGT

28

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGAAAGGGT CCCTCCTGCT GCTGCT

26

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TATCAGCTCC ATGCCCTCTA GAAGCC

26

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Jonathan A. Bard, et al.
 Serial No. : 09/058,333
 Filed : April 9, 1998
 For : DNA ENCODING GALANIN GALR3 RECEPTOR AND USES
 THEREOF

10/007132
 12/03/01
 JC675 U.S. PTO

1185 Avenue of the Americas
 New York, New York 10036
 August 3, 1998

Assistant Commissioner for Patents
 Washington, D.C. 20231
 Box: Missing Parts

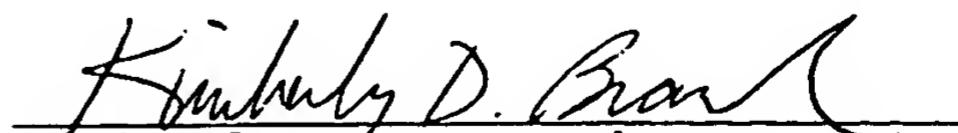
Sir:

STATEMENT IN ACCORDANCE WITH 37 C.F.R. §1.821(f)

In accordance with 37 C.F.R. §1.821(f), I hereby certify that the computer readable form containing the nucleic acid and/or amino acid sequences required by 37 C.F.R. §1.821(e) and submitted in connection with the above-identified application, has the same information as replacement pages 171-194 of the subject application entitled "Sequence Listing."

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these were made with the knowledge that wilful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such wilful false statements may jeopardize the validity of the application or any patent issued thereon.

Respectfully submitted,


 Kimberly D. Branch
 c/o Cooper & Dunham LLP
 1185 Avenue of the Americas
 New York, New York 10036
 (212) 278-0400

Applicants: Jonathan A. Bard et al.
 Serial No: Not Yet Known
 Filed: Herewith
Exhibit 3

ATCC

10801 University Blvd • Manassas, VA 20110-2209 • Telephone: 703-365-2700 • FAX: 703-

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE

10/00/7132
12/03/01
JC675 U.S. PTO

INTERNATIONAL FORM

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT ISSUED PURSUANT TO RULE 7.3 AND VIABILITY STATEMENT ISSUED PURSUANT TO RULE 10.2

To: (Name and Address of Depositor or Attorney)

Cooper & Dunham LLP
Attn: John P. White, Esq.
1185 Avenue of the Americas
New York, NY 10036

COPY

Deposited on Behalf of: Synaptic Pharmaceutical Corporation (Docket 52241-E)

Identification Reference by Depositor:

ATCC Designation

Plasmid M67 209708

The deposit was accompanied by: a scientific description a proposed taxonomic description indicated above.

The deposit was received March 27, 1998 by this International Depository Authority and has been accepted.

AT YOUR REQUEST: We will inform you of requests for the strain for 30 years.

The strain will be made available if a patent office signatory to the Budapest Treaty certifies one's right to receive, or if a U.S. Patent is issued citing the strain, and ATCC is instructed by the United States Patent & Trademark Office or the depositor to release said strain.

If the culture should die or be destroyed during the effective term of the deposit, it shall be your responsibility to replace it with living culture of the same.

The strain will be maintained for a period of at least 30 years from date of deposit, or five years after the most recent request for a sample, whichever is longer. The United States and many other countries are signatory to the Budapest Treaty.

The viability of the culture cited above was tested April 8, 1998. On that date, the culture was viable.

International Depository Authority: American Type Culture Collection, Manassas, VA 20110-2209 USA.

Signature of person having authority to represent ATCC:

Barbara M. Hailey
Barbara M. Hailey, Administrator, Patent Depository

Date: April 22, 1998

cc: Kimberly Branch

Applicants: Jonathan A. Bard et al.
Serial No: Not Yet Known
Filed: Herewith
Exhibit 4

Form PTO-1449		U.S. Department of Commerce Patent and Trademark Office		Atty. Docket No. 52241-EC /JPW/ADM/PL	Serial No. Not Yet Known
INFORMATION DISCLOSURE CITATION BY APPLICANT (Use several sheets if necessary)				Applicant Jonathan A. Bard, et al.	
		Filing Date Herewith	Group		

JC 675 U.S. PRO
 10/007132
 12/03/01

U.S. PATENT DOCUMENTS

Examiner Initial		Document Number		Date	Name	Class	Subclass	Filing Date if Appropriate						
		5	2	9	0	8	0	8	3/1/94	Sofia, et al.				
		5	4	3	6	1	2	8	7/25/95	Harpold, et al.				
		5	4	3	6	1	5	5	7/25/95	Bell, et al.				
		5	4	6	2	8	5	6	10/31/95	Lerner, et al.				
		5	5	0	8	1	6	4	4/16/96	Kausch, et al.				
		5	5	6	7	7	1	4	10/22/96	Bruns, et al.				
		5	5	7	6	2	9	6	11/29/96	Bartfai, et al.				

FOREIGN PATENT DOCUMENTS

		Document Number		Date	Country	Class	Subclass	Translation						
								Yes	No					
		9	9	3	1	1	3	0	6/24/99	PCT				
		9	2	1	5	6	8	1	9/17/92	PCT				
		9	8	0	3	5	4	8	1/29/98	PCT				
		9	8	0	3	0	5	9	1/29/98	PCT				

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, Etc.)

	Ahmad, A., et al., Identification And Molecular Cloning Of A Novel Galanin Receptor (GALR-2) In Rat Sensory Neurons, <i>Soc. Neurosci. Abstr.</i> , 1996, <u>22</u> (3): 1682, Abst. No. 661.10;
	Ahmad, S. et al., Molecular Cloning of a Novel Widely Distributed Galanin Receptor Subtype (GALR2), <i>International Association for the Study of Pain (IASP Press)</i> , 1996, Abstract No. <u>81</u> : 134;
	Ahmad, S. et al., Astra Pain Control, 1996, poster;
	Bartfai, T., et al., Galanin Receptor Ligand M40 Peptide Distinguishes Between Putative Galanin-Receptor Subtypes, <i>PNAS USA</i> , 1993, <u>90</u> : 11287-11291;

EXAMINER	DATE CONSIDERED

*EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609: Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

Applicants: Jonathan A. Bard et al.
 Serial No: Not Yet Known
 Filed: Herewith
Exhibit 5

Form PTO-1449		U.S. Department of Commerce Patent and Trademark Office		Atty. Docket No. 52241-EC /JPW/ADM/PL	Serial No. Not Yet Known
INFORMATION DISCLOSURE CITATION BY APPLICANT (Use several sheets if necessary)				Applicant Jonathan A. Bard, et al.	
		Filing Date Herewith	Group		

FOREIGN PATENT DOCUMENTS

		Document Number	Date	Country	Class	Subclass	Translation	
							Yes	No
		9 2 1 2 9 9 7	8/6/92	PCT				
		9 2 1 5 0 1 5	9/3/92	PCT				
		9 5 2 2 6 0 8	8/24/95	PCT				
		9 7 4 6 6 8 1	12/11/97	PCT				
		5 1 4 3 6 1	11/19/92	EPO				
		7 1 1 8 3 0	5/15/96	EPO				

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	Bouvier, M. et al., Dynamic Palmitoylation of G-Protein-Coupled Receptors in Eukaryotic Cells, <i>Methods in Enzymology</i> , 1995, 250: 300-314;
	Bowie, et al., Deciphering the message in protein sequences: tolerance to amino acid substitutions, <i>Science</i> , 1990, 247: 1306-1310;
	Burgevin, M.C., et al., Cloning, Pharmacological Characterization and Anatomical Distribution of a Rat cDNA Encoding for a Galanin Receptor, <i>J. Molec. Neurosci.</i> , 1995, 6: 33-41;
	Chen, Y. et al., Purification of a Galanin Receptor From Pig Brain, <i>PNAS USA</i> , 1993, 90: 3845-3849;
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